WHAT IS CLAIMED IS:

1. An isolated enone reductase having the physicochemical properties of (A)-(C):

(A) it reduces the carbon-carbon double bond of an α,β-unsaturated ketone, using NADPH as an electron donor, to produce a corresponding saturated hydrocarbon;

(B) it has a substrate specificity of (1)-(4):

(1) it has substantially no activity to reduce the keto group of a ketone;

(2) it exhibits a significantly higher activity with NADPH than with NADH as an electron donor;

(3) it does not substantially act on substrates wherein both substituents at the β carbon relative to the ketone are not hydrogen; and

(4) it does not substantially act on a substrate in which the carbon-carbon double bond is present in a cyclic structure; and

(C) it has an optimal pH of 6.5-7.0.

2. The enone reductase of claim 1, wherein the reductase (a) has an optimum temperature of 37-45°C; and (b) has a molecular weight determined by sodium dodecyl sulfate-polyacrylamide gel electrophoresis and by gel filtration of about 43,000 and about 42,000, respectively.

3. The enone reductase of claim 1, which is derived from an organism of the genus *Kluyveromyces*.

4. A method for obtaining an enone reductase, comprising the step of (a) culturing a microorganism belonging to the genus *Kluyveromyces*; and (b) isolating the enone reductase of claim 1 from the cultured microorganism.

5. The method of claim 4, wherein the microorganism belonging to the genus *Kluyveromyces* is *Kluyveromyces lactis*.

6. An isolated nucleic acid of any one of (a) to (d) below:

(a) a nucleic acid encoding a protein comprising the amino acid sequence of SEQ ID NO:2;

(b) a nucleic acid comprising a coding region of the nucleotide sequence of SEQ ID NO:1;

(c) a nucleic acid encoding a protein that comprises the amino acid sequence of SEQ ID NO: 2, in which one or more amino acids are substituted, deleted, inserted and/or added and that is functionally equivalent to a protein consisting of the amino acid sequence of SEQ ID NO: 2;

(d) a nucleic acid that hybridizes under stringent conditions with a nucleic acid consisting of the nucleotide sequence of SEQ ID NO: 1, and that encodes a protein functionally equivalent to a protein consisting of the amino acid sequence of SEQ ID NO:2; and

(e) a nucleic acid encoding a protein that has at least 60% identity to the amino acid sequence of SEQ ID NO:2.

7. An isolated nucleic acid encoding the amino acid sequence of SEQ ID NO:2 or a fragment thereof.

8. A vector comprising the nucleic acid of claim 6.

9. A vector comprising the nucleic acid of claim 7.

10. The vector of claim 8, further comprising a nucleic acid sequence encoding a dehydrogenase that catalyzes oxidation-reduction reactions using NADP as a coenzyme.

11. The vector of claim 9, further comprising a nucleic acid sequence encoding a dehydrogenase that catalyzes oxidation-reduction reactions using NADP as a coenzyme.

12. A transformant harboring the nucleic acid of claim 6.

13. A transformant harboring the nucleic acid of claim 7.

14. A transformant harboring the vector of claim 8.

15. A transformant harboring the vector of claim 10.

16. A substantially purified polypeptide encoded by the nucleic acid of claim 6.

17. A substantially purified polypeptide encoded by the nucleic acid of claim 7.

18. A method for producing a polypeptide, the method comprising the steps of culturing the transformant of claim 12 and recovering a polypeptide expressed from the transformant or the culture supernatant thereof.

19. A method for producing a polypeptide, the method comprising the steps of culturing the transformant of claim 13 and recovering a polypeptide expressed from the transformant or the culture supernatant thereof.

20. A method for producing a polypeptide, the method comprising the steps of culturing the transformant of claim 14 and recovering a polypeptide expressed from the transformant or the culture supernatant thereof.

21. A method for producing a polypeptide, the method comprising the steps of culturing the transformant of claim 15 and recovering a polypeptide expressed from the transformant or the culture supernatant thereof.

22. An isolated nucleic acid of any one of (a) to (d) below:

(a) a nucleic acid encoding a protein comprising the amino acid sequence of SEQ ID NO:4, 6 or 8;

(b) a nucleic acid comprising a coding region of the nucleotide sequence of SEQ ID NO:3, 5 or 7;

(c) a nucleic acid encoding a protein that comprises the amino acid sequence of SEQ ID NO:4, 6 or 8 in which one or more amino acids are substituted, deleted, inserted and/or added and that is functionally equivalent to a protein consisting of the amino acid sequence of SEQ ID NO:4, 6 or 8;

(d) a nucleic acid that hybridizes under stringent conditions with the nucleic acid consisting of the nucleotide sequence of SEQ ID NO: 3, 5 or 7, and that encodes a protein functionally equivalent to a protein consisting of the amino acid sequence of SEQ ID NO:4, 6 or 8; and

(e) a nucleic acid encoding a protein that has at least 60% identity to the amino acid sequence of SEQ ID NO:4, 6 or 8.

23. A substantially purified polypeptide encoded by the nucleic acid of claim 22.

24. A vector comprising the nucleic acid of claim 22.

25. The vector of claim 24, further comprising a nucleic acid sequence encoding a dehydrogenase that catalyzes oxidation-reduction reactions using NADP as a coenzyme.

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26. A transformant harboring the nucleic acid of claim 2.

27. A transformant harboring the vector of claim 24.

28. A transformant harboring the vector of claim 25.

29. A method for producing a polypeptide, the method comprising the steps of culturing the transformant of claim 26 and recovering a polypeptide expressed from the transformant or the culture supernatant thereof.

30. A method for producing a polypeptide, the method comprising the steps of culturing the transformant of claim 27 and recovering a polypeptide expressed from the transformant or the culture supernatant thereof.

31. A method for selectively reducing the carbon-carbon double bond of an α,β-unsaturated ketone, comprising the step of reacting an α,β-unsaturated ketone with the enone reductase of claim 1.

32. A method for selectively reducing the carbon-carbon double bond of an α,β-unsaturated ketone, comprising the step of reacting an α,β-unsaturated ketone with the polypeptide of claim 16.

33. A method for selectively reducing the carbon-carbon double bond of an α,β-unsaturated ketone, comprising the step of reacting an α,β-unsaturated ketone with the polypeptide of claim 17.

34. A method for selectively reducing the carbon-carbon double bond of an α,β-unsaturated ketone, comprising the step of reacting an α,β-unsaturated ketone with the polypeptide of claim 23.

35. A method for selectively reducing the carbon-carbon double bond of an α,β-unsaturated ketone, comprising the step of reacting an α,β-unsaturated ketone with a microorganism that produces an enone reductase having the physicochemical properties of (A)-(C):

(A) it reduces the carbon-carbon double bond of an α,β-unsaturated ketone, using NADPH as an electron donor, to produce a corresponding saturated hydrocarbon;

(B) it has a substrate specificity of (1)-(4):

(1) it has substantially no activity to reduce the keto group of a ketone;

(2) it exhibits a significantly higher activity with NADPH than with NADH as an electron donor;

(3) it does not substantially act on substrates wherein both substituents at the β carbon relative to the ketone are not hydrogen; and

(4) it does not substantially act on a substrate in which the carbon-carbon double bond is present in a cyclic structure; and

(C) it has an optimal pH of 6.5-7.0.

36. The method of claim 35, wherein the microorganism is of the genus *Kluyveromyces*.

37. The method of claim 35, wherein the microorganism is the transformant of claim 12.

38. The method of claim 35, wherein the microorganism is the transformant of claim 26.

39. A method for selectively reducing the carbon-carbon double bond of an α,β-unsaturated ketone, comprising the step of reacting an α,β-unsaturated ketone with a processed product of a microorganism that produces an enone reductase having the physicochemical properties of (A)-(C):

(A) it reduces the carbon-carbon double bond of an α,β-unsaturated ketone, using NADPH as an electron donor, to produce a corresponding saturated hydrocarbon;

(B) it has a substrate specificity of (1)-(4):

(1) it has substantially no activity to reduce the keto group of a ketone;

(2) it exhibits a significantly higher activity with NADPH than with NADH as an electron donor;

(3) it does not substantially act on substrates wherein both substituents at the β carbon relative to the ketone are not hydrogen; and

(4) it does not substantially act on a substrate in which the carbon-carbon double bond is present in a cyclic structure; and

(C) it has an optimal pH of 6.5-7.0.

40. The method of claim 38, wherein the microorganism is of the genus *Kluyveromyces*.

41. The method of claim 38, wherein the microorganism is the transformant of claim 12.

42. The method of claim 38, wherein the microorganism is the transformant of claim 26.